Combining Ability And Nature of Gene Effects Controlling Seed Yield And Its Component Traits In Alien Cytoplasm Based Hybrids In Sunflower (*Helianthus Annuus L.*)

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Abstract

The present research aimed to study gene effects for seed yield and its component traits in sunflower hybrids having diverse cytotsterile sources from *Helianthus annuus* and *H. argophyllus*. Five lines and ten testers were crossed in a line x tester mating design to develop 50 F₁ hybrids for genetic analysis. The analysis of variance revealed significant differences among the traits studied. Seasonal variation was found significant for all the traits except stem diameter, volume weight and seed filling percentage. The mean squares of lines and testers from crosses both determine the GCA were also significant for most of the traits which revealed the prevalence of additive variances and additive gene action. The mean squares of lines x tester interactions were also significant for all the traits considered. The significance of lines x tester interactions indicated that SCA is also important in the expression of traits and demonstrated the value of non-additive variances and dominant genes controlling the various traits. Among the diverse cytotsterile lines, ARG-6-3-1-4 was identified as the best general combiner for stem diameter, volume weight, seed yield, hull content, oil content and oil yield. While, the line ARG-2-1-2 was best general combiner for days to 50 per cent flowering, head diameter, 100 seed weight and seed filling percentage. The tester M17-R was observed to be best general combiner for earliness and volume weight, while RHA 93 was the best general combiner for plant height, seed yield and oil content. The best cross combinations; MUT-2-8-3-2 x GKVK 3 was found to be good specific combiner for stem diameter, 100 seed weight, seed yield, seed filling percentage, oil content and oil yield, while ARG-6-3-1-4 x GKVK 3 was good specific combiner for days to 50% flowering, plant height and 100 seed weight.

Introduction

Sunflower is an oilseed crop used for edible purpose and other industrial use. The crop is grown globally and performs well in almost all continents where it is grown. Sunflower was introduced to India during 1969 from Russia in view of its distinct advantages, viz., photo insensitivity, short duration, high seed multiplication ratio, high seed yield and better quality of oil. However, commercial cultivation of sunflower in India started during 1972 with the introduction of Russian varieties. A major event in sunflower history was the discovery of cytoplasmic male sterility (CMS) in a wild prairie sunflower, *Helianthus petiolaris* Nutt. (Leclercq, 1969), and subsequent identification of genes for fertility restoration by Kinman (1970); Enns et al. (1970), Leclercq (1971) and Vranceanu and Stoenescu (1971) that led to the production of commercial hybrids. Sunflower hybrids are preferred over varietal populations as hybrids offer several benefits in terms of growth, development, synchronous flowering, early maturity, higher seed setting, increased productivity, resistance to major foliar diseases and also respond to higher level of chemical fertilizer application. In India the first ever CMS based sunflower hybrid BSH-1 was released from the University of Agricultural Sciences, Bangalore (Seetharam et al. 1980) which provided the required fillip to expand sunflower cultivation in the country. Since then, many hybrids have been released for commercial cultivation by utilizing cytoplasmic genetic male sterility system. The area under sunflower in India was 0.25 million hectares with a production of 0.22 million tones and productivity of 0.9 t/ha (Anonymous, 2019). Over 70% of the sunflower crop is being grown across the states of Karnataka, Maharashtra and Andhra Pradesh. In Karnataka it occupies an area of about 1.60 lakh ha. with a production of 1.20 lakh tonnes and productivity of 0.75 t/ha. Karnataka, popularly known as the “Sunflower State” in the oilseed scenario of the country, occupies first position, accounting for 63% of the total acreage and contributing to 53% of the national sunflower production.

Much of the current germplasm used in sunflower breeding programs originated from limited genetic material, resulting in a crop with an extremely narrow genetic base. At present, only one CMS source (i.e., PET-1) is being widely used for sunflower hybrid breeding program (Seiler et al. 2017). This cytoplasmic uniformity poses a potential risk for hybrid sunflower production. Prevalence of genetic uniformity of this kind over a large area could result in genetic vulnerability of hybrids if the cytoplasm becomes susceptible to a new strain of disease or pest similar to that happened in maize when ‘Texas’ cytoplasm become susceptible to *Helminthosporium maydis* in USA (Tatum, 1971). Among several strategies available to overcome this problem, diversification of CMS source itself is possibly the cheapest and most effective method. The utilization of different cytoplasmic backgrounds in hybrid development will improve the general variability of sunflower plants and lessen the threats of epiphytotics.

Combining ability studies elucidate the nature and magnitude of gene action involved in the inheritance of character by providing the information on additive and dominance genetic variance. The estimates of general combining ability forms the basis to select parents while, specific combining ability depicts the worth of hybrids. Sunflower, being a highly cross pollinated crop is ideally suited for exploitation of heterosis. Several biometrical methods have been developed to generate information on gene action and mode of inheritance of various characters among which Line x Tester analysis (Kempthorne, 1957) is widely used method in genetic analysis in large number of crops. The GCA is the average performance of a particular inbred in a series of hybrid combinations, whereas SCA refers to the performance of a combination of specific inbred in a particular cross (Sprague and Tatum, 1942). The GCA and SCA variances provide an estimation for additive and non-additive gene actions, respectively (Falconer, 1967). In sunflower, various reports indicated the importance of both additive and non-additive genetic variances for yield and other characters (Memon et al. 2015; Riaz et al., 2017; Tyagi and Dhillon. 2017; Lakshman et al. 2019). The objectives of present research therefore were aimed at determining the potentiality of five alloplasmic female lines having cytotsterility source from *Helianthus annuus* and *Helianthus argophyllus* and ten testers for developing 50 sunflower alloplasmic hybrids and to estimate the role of additive and non-additive genes so as to design breeding experiments to improve seed yield and its component traits and to expand the cytoplasmic base of sunflower hybrids.

Materials And Methods

The present investigations were undertaken at the Zonal Agricultural Research Station, Univeristy of Agricultural Sciences, Gandhi Krishi Vigyana Kendra, Bangalore, India. The research station is geographically situated at 12°58' N latitude and 77°35' N longitude at an altitude of 930 meters above mean sea level. Materials for the study consisted of five male sterile lines viz., ARG-2-1-2, MUT-2-8-3-2, E002, ARG 3 and ARG-6-3-1-4 (Fig 1-5) developed from diverse cytoplasmic male sterile sources in different nuclear genetic background (Table 1) and ten restorers/testers viz., GKVK-3, RHA 6D-1, RHA 95-C-1, LTRR 822, M-17R, MR-1, RHA-272-II, X-15-NB-10, GKVK-2 and RHA-93. The list of five diversified CMS lines with their origin is furnished below.

Table 1. Diversified CMS Lines

SI No	CMS designation	Cytosterility source	Nuclear Genetic background
1	ARG-2-1-2	<i>H. argophyllus</i>	234
2	MUT-2-8-3-2	<i>H. annuus</i>	234
3	E002	<i>H. annuus</i>	DS2
4	ARG 3	<i>H. argophyllus</i>	DS2
5	ARG-6-3-1-4	<i>H. argophyllus</i>	REC 428

During *Rabi* – 2015-16, all the diverse CMS lines and 10 restorer lines were sown in the field to effect crossing in Line × Tester fashion. Staggered sowing of all inbred lines was carried out three times at an interval of two days to ensure flowering synchronization with diverse CMS lines. In order to prevent undesirable pollination, heads of CMS lines were covered with cloth bags a day prior to opening of first ray floret. Similarly, the capitula of inbred lines were also covered with cloth bags to collect pollen. Pollen from the inbred lines were collected in petri plates and applied to the flowers of female lines using camel hairbrush during morning hours. The pollination was repeated for five to six days in each of the combination to ensure sufficient seed set and simultaneously, all inbreds were sib pollinated. At maturity, the crossed seeds of 50 combinations were collected for future evaluation. Hybrids were evaluated in *Kharif* 2016 and *Rabi/Summer* 2016-17 with two replications each and experiment was laid out in randomized block design (Fig. 6). Each genotype was sown in a single row of three meter length with spacing of 60 cm and 30 cm between plants and within row respectively. All the recommended practices were followed for raising successful crop under protective irrigated condition. The data during germination till maturity were obtained from F₁ plants and their parents for days to 50% flowering, plant height (cm), head diameter (cm), stem diameter (cm), days to maturity, 100-seed weight (g), volume weight (g 100ml⁻¹), seed yield (kg ha⁻¹), hull content (%), seed filling percentage, oil content (%) and oil yield (kg ha⁻¹). The seed oil content was determined by nuclear magnetic resonance spectrometry (NMRS). The data were analyzed for determining the differences among genotypes, parents, crosses, parents vs. crosses according to Gomez and Gomez (1984), while mean squares for GCA were determined from lines and testers and specific combining ability from lines x tester interactions according to statistical procedures developed by Kempthorne (1957) and adopted by Singh and Choudhary (1984).

Results And Discussion

Pooled analysis of variance

Presence of genetic variability is the basic requirement for developing high yielding hybrids in sunflower breeding programme. Pooled analysis of variance for experimental design shown in table 2, indicated significant differences among genotypes, parents and crosses for all the studied traits confirming that the data is worth for genetic analysis.

The pooled analysis of variance for combining ability due to different source for twelve characters (table 3) revealed that seasonal variation was significant for all the traits except stem diameter, volume weight and seed filling percentage. The mean squares of lines and testers from crosses both determine the GCA were also significant for most of the traits which revealed the prevalence of additive variances and additive gene action. The mean squares of lines x tester interactions were significant for all the traits considered. The significance of lines x tester interactions indicated that SCA is also important in the expression of traits and demonstrated the value of non-additive variances and dominant genes controlling the above traits. Memon et al. (2015), Lakshman et al. (2019) and Hilli et al. (2020) also observed that both additive and non-additive genetic variations were equally important for yield and its contributing traits in sunflower.

Table 2: Pooled Analysis of variance for seed yield and its attributing traits in sunflower.

Source of Variations	d.f	Days to 50% flowering	Plant height (cm)	Head diameter (cm)	Stem diameter (cm)	Days to Maturity	100 seed weight (g)	Volume weight (g/100ml)	Seed yield (kg/ha)	Hull content (%)	Seed filling percent	Oil content (%)
Replicates	1	0.65	87.08	2.94	0.05	3.02	0.05	2.66	171553.20	20.28	9.89	1.00
Season	1	973.11**	6509.30**	18.72**	0.07**	1024.06**	16.18**	17.86*	1000458.85**	138.82**	0.0002	4.00
Genotypes	64	29.22**	1411.20**	7.97**	0.15**	40.95**	1.64**	27.02**	1321399.76**	34.35**	37.25**	4.00
Crosses	49	22.74**	558.12**	1.05**	0.05**	34.67**	0.69**	29.43**	147303.15**	30.69**	37.99**	4.00
Hybrids	36	4.66**	184.93**	0.84**	0.04**	12.42**	0.48**	6.71**	99531.47**	22.14**	21.65	1.00
Parents vs Crosses	1	21.34**	25165.55**	204.28**	3.74**	4.02	25.37**	35.51**	54769267.49**	316.93**	190.94**	4.00
Error	128	1.08	47.47	0.21	0.01	1.70	0.08	3.29	36192.46	0.92	1.77	1.00

** Significant at P ≤ 0.01

*Significant at P ≤ 0.05

Table 3: Pooled Analysis of variance for combining ability for seed yield and its attributing traits in sunflower.

Source of Variations	d.f	Days to 50% flowering	Plant height (cm)	Head diameter (cm)	Stem diameter (cm)	Days to maturity	100 seed weight (g)	Volume weight (g/100ml)	Seed yield (kg/ha)	Hull content (%)	Seed filling percent
Replicates(R)	1	1.280	0.551	1.84	0.03	1.45	0.048	10.37	289205.52	29.28**	28.74
Season(S)	1	1003.52**	12987.88**	1.51**	0.002	804.01**	12.370**	4.14	9889505.58**	140.47**	0.05
R X S	1	0.02	3191.21**	1.28*	0.002	1.13	0.094	53.54**	48921.94	6.65**	0.42
Crosses (C)	49	22.74**	558.12**	1.05**	0.05**	34.67**	0.686**	29.43**	147303.15**	30.69**	37.99**
Lines (L)	4	80.04**	2723.99**	1.67	0.03	111.79**	2.301**	101.65**	341161.03*	103.75**	131.40**
Tester (T)	9	69.62**	1088.27**	1.61	0.10*	89.41**	0.790	88.19**	252230.83*	32.48	61.86*
Lines X Tester	36	4.66**	184.93**	0.84**	0.04**	12.42**	0.481**	6.71**	99531.47**	22.14**	21.65**
S X C	49	2.64*	132.63**	0.42**	0.003	5.64**	0.043	1.42	24376.23	1.14	1.31
S X L	4	3.66	124.19	0.29	0.002	1.22	0.02	11.84**	40277.69	0.23	1.45
S X T	9	4.63*	168.23	0.68	0.001	9.03	0.07	0.51	42703.38*	1.01	0.85
S X LxT	36	2.03*	124.67**	0.37*	0.001	5.28**	0.03	0.48	18027.61	1.27	1.40
Error	98	1.15	41.21	0.20	0.007	2.04	0.083	3.21	44015.29	0.88	1.32

** Significant at $P \leq 0.01$

*Significant at $P \leq 0.05$

Table 4: Estimates of general combining ability effects of lines for seed yield and its attributes in sunflower

Lines	Days to 50% flowering	Plant height (cm)	Head diameter (cm)	Stem diameter (cm)	Days to maturity	100 seed weight (g)	Volume weight (g/100ml)	Seed yield (Kg/ha)	Hull content (%)	Seed filling percent	Oil content (%)	Oil yield (Kg/ha)
ARG-2-1-2	-1.670**	4.088**	0.270**	0.0001	2.580 **	0.363 **	0.473	93.574 **	-0.969 **	1.686 **	2.571 **	83.189 **
MUT-2-8-3-2	0.155	4.430**	-0.075	-0.005	0.670 **	0.046	1.019 **	-60.981	-0.190	0.523 **	-3.967 **	-98.022 **
E002	-0.995**	-5.713**	-0.035	-0.008	-0.630 **	-0.211 **	-1.869 **	-50.603	1.465 **	0.377 *	0.444 **	-12.490
ARG 3	0.530**	-11.390**	-0.272**	-0.029 *	0.795 **	-0.225 **	-1.446 **	-88.253 **	1.745 **	-3.101 **	-2.688 **	-83.452 **
ARG-6-3-1-4	1.980**	8.585**	0.113	0.041 **	1.745 **	0.027	1.822 **	106.263 **	-2.051 **	0.515 **	3.640 **	110.775 **
SE ±	0.170	1.015	0.071	0.013	0.226	0.046	0.283	33.172	0.148	0.182	0.065	11.268

** Significant at $P \leq 0.01$

*Significant at $P \leq 0.05$

Table 5: Estimates of general combining ability effects of testers for seed yield and its component traits in sunflower.

Testers	Days to 50% flowering	Plant height (cm)	Head diameter (cm)	Stem diameter (cm)	Days to maturity	100 seed weight (g)	Volume weight (g/100ml)	Seed yield (Kg/ha)	Hull content (%)	Seed filling percent	Oil content (%)	Oil yield (Kg/ha)
GKVK-3	3.480**	-1.608	-0.100	0.042 *	3.695 **	0.232 **	2.071 **	88.047	-0.088	1.654 **	-0.605 **	13.298
RHA-6D-1	0.880**	1.233	0.135	-0.003	1.845 **	-0.080	0.245	-89.587	-1.053 **	1.047 **	0.870 **	-11.862
RHA-95-C-1	1.730**	13.943**	0.545**	0.106 **	2.095 **	0.184 **	0.703	72.991	-0.261	1.277 **	0.942 **	44.960 **
LTRR-822	1.730**	5.662**	0.055	0.054 **	1.145 **	0.021	-3.152 **	13.824	-2.018 **	-0.755 **	0.088	8.946
M17-R	-2.120**	-3.093**	-0.410**	-0.074 **	-2.805 **	-0.440 **	3.166 **	-133.831 **	-0.646 **	-0.732 **	0.210 *	-42.453 **
MR-1	-1.270**	0.663	0.125	0.052 **	-0.855 **	-0.117	0.145	105.547 *	0.367	1.182 **	0.279 **	41.580 *
RHA-272-II	-1.470**	-1.077	0.235*	-0.002	-1.955 **	0.198 **	-0.505	-159.909 **	2.121 **	-3.848 **	-1.152 **	-77.819 **
X-15-NB-10	-0.070	0.093	-0.070	0.028	-0.105	-0.092	-3.161 **	-75.009	1.113 **	1.187 **	0.201 *	-24.241
GKVK-2	-1.520**	-0.068	-0.355**	-0.116 **	-1.955 **	0.023	1.745 **	-0.842	1.451 **	-1.760 **	0.281 **	6.896
RHA-93	-1.370**	-15.748	-0.160	-0.086 **	-1.105 **	0.073	-1.256 **	178.769 **	-0.984 **	0.748 **	1.115 **	40.695 *
SE±	0.240	1.435	0.101	0.019	0.319	0.064	0.401	46.912	0.210	0.257	0.092	15.936

** Significant at ≤ 0.01

* Significant at ≤ 0.05

General combining ability effects

Combining ability of a line/strain to produce superior progenies upon hybridization with other lines/strains is an important criteria to select parents for developing superior new hybrids. To reduce the crop growth period, lesser number of days to flowering and maturity is preferred. The sunflower growers require short duration hybrids, because such hybrids reduce the incidence of insect-pest, disease attack and adverse environmental effects (Memon et al. 2015). For days to 50% flowering and days to maturity only line E002 exhibited significant negative *gca* effect (table 4) for both these traits while among testers highest significant negative *gca* effect was recorded by M17-R (table 5) for both the traits followed by GKVK 2 and RHA-272-II. Thus the lines E002 and testers M17-R, GKVK 2 and RHA-272-II were found to be good general combiners for earliness. Therefore, these lines could be used in the synthesis of early maturing hybrids. Meena et al. (2013) and Azad et al. (2016) have also identified good general combiners for early flowering.

As reduced plant height promotes resistant to lodging, there is also a huge interest in the development of semi-dwarf hybrids. The most prominent negative effect of the GCA for plant height was found in the CMS lines in ARG 3 (-11.390) and for the same traits among the testers in RHA-93 (-15.748), hence, the lines and testers with negative *gca* effects can be used in hybridization programme to synthesize medium stature plants. For head diameter, line ARG-2-1-2 (0.270) exhibited significant positive *gca* effects while line ARG 3 (-0.272) exhibited significant negative *gca* effect while among testers, only RHA-95-C-1 (0.545) and RHA 272-II (0.235) exhibited significant positive *gca* effect. Riaz et al. (2017) have also reported similar results and inferred that these identified lines and testers with positive *gca* effect could be used in further breeding programme to synthesis hybrids with large head size thus intern contributing to increased yield. For stem diameter lines ARG-6-3-1-4 (0.041) exhibited highest significant positive effect and ARG 3 (-0.029) exhibited significant negative *gca* effect. Testers RHA-95-C-1 (0.106) followed by MR-1 (0.052) exhibited highest significant positive *gca* effect as also observed in the studies of Lakshman et al. (2019) indicating the preponderance of additive effect in the inheritance of this character.

The seed weight of a genotype serves as an indicator to the expression of an end product i.e., seed yield as it is an important character contributing to seed yield. Lines ARG-2-1-2 (0.363) exhibited highest significant positive *gca* effect while testers viz., GKVK 3 (0.232), RHA 272-II (0.198) and RHA-95-C-1 (0.184) registered significant positive *gca* effect indicating their high utility in the breeding programme. For volume weight lines ARG-6-3-1-4 (1.822) and MUT-2-8-3-2 (1.019) exhibited significant positive *gca* effect. Three testers expressed significant positive *gca* effect, highest being manifested by M17-R (3.166) followed by GKVK 3 (2.071) and GKVK-2 (1.745). Hence, these lines and testers showing positive *gca* effects could be used in hybridization programme to develop hybrids with high seed weight and volume weight. Patil et al. (2012) have also reported good general combiners for these yield attributing traits.

The *gca* effects for seed yield varied both in magnitude and direction among both lines and testers. Lines ARG-6-3-1-4 (106.263) and ARG-2-1-2 (93.574) expressed significant positive *gca* effects while, ARG 3 (-88.253) exhibited significant negative *gca* effect. Among testers *gca* effects ranged from 178.769 (RHA 93) to -159.909 (RHA 272-II). Only one tester recorded positive *gca* effect and two recorded negative *gca* effects. It was interesting to note that the line ARG-6-3-1-4 is good general combiners for most of the yield contributing characters, showing that a positive association exists between seed yield and its attributes such as plant height, stem diameter, head diameter and volume weight. Hence, ARG-6-3-1-4 could also be used in breeding for development of

hybrids with higher seed yield. In earlier reports, Salem and Ali (2012), Memon et al. (2015) and Chahal et al. (2019) have also reported good general combiners for seed yield. Patil et al. (2012) in their study observed significant *gca* effects for hull content. In our results also lines ARG-6-3-1-4 (-2.051) and ARG-2-1-2 (-0.969) exhibited significant negative *gca* effect which is desirable. Four of the ten testers registered significant negative *gca* effect, highest being recorded by LTRR 822 (-2.018) followed by RHA 6D-1 (-1.053) and M17-R (-0.646). Parents showing negative *gca* for this trait can be considered to develop hybrids having low hull content. For seed filling percentage lines ARG-2-1-2 (1.686), MUT-2-8-3-2 (0.523), ARG-6-3-1-4 (0.515) and E002 (0.377) exhibited significant positive *gca*. whereas, line ARG 3 (-3.101) exhibited significant negative *gca* effect. All the testers, recorded significant *gca* effect, with six being positive and four being negative. Highest positive being recorded by GKVK 3 (1.654) followed by RHA-95-C-1 (1.277). Lakshman et al. (2019) have reported similar results for seed filling percentage inferring that the lines and tester having positive significant *gca* effects appeared to transmit the increasing alleles with additive effects.

As Sunflower is an oilseed crop, oil is the ultimate end product and hence, increase in oil content is of prime most important. All the lines tested expressed significant *gca* effects of which three of them were positive and two of them were negative. The line ARG-6-3-1-4 (3.640) manifested the highest positive significant *gca* effect followed by ARG-2-1-2 (2.571) and E002 (0.444). Seven testers registered significant positive *gca* effect. The testers RHA-93 (1.115) followed by RHA 95-C-1 (0.942) and RHA 6D-1 (0.870) were the best general combiners for oil yield. Similar findings for oil content were reported by Azad et al. (2016) and Attia et al. (2020). Oil yield is a derivative trait of oil content and seed yield. Good general combiners for this trait have been identified in earlier works of Lakshman et al. (2019) and Hilli et al. (2020). In the present study except ARG 3, all lines exhibited significant *gca* effect, highest significant positive *gca* effect is being manifested by ARG-6-3-1-4 (110.775) followed by ARG-2-1-2 (83.189). Among the testers, highest significant positive *gca* being manifested by RHA-95-C-1 (44.960) followed by MR-1 (41.580) and RHA-93 (40.695). On the contrary, highest negative *gca* effect registered by RHA 272-II (-77.819) followed by M17-R (-42.453). Kaya and Atakisi (2004) reported that superior hybrids were obtained by crossing CMS females and restorer males with high GCA and SCA effects. On the similar lines, ARG-6-3-1-4 and ARG-2-1-2 and testers RHA-95-C-1, MR-1 and RHA-93 with high positive GCA estimates can be desirable parents to be used for developing sunflower hybrids with improved oil yield.

Specific combining ability effects

The relative performance of any cross combination is expressed as specific combining ability and is denoted in terms of *sca* effects and SCA variance. The SCA variance denotes non additive or dominance portion of variance and generally non fixable on selfing but can be exploited in hybrid combination. Out of 50 crosses, only 5 hybrids recorded the desirable significant negative *sca* effects and 3 hybrids exhibited significant positive *sca* effects for days to 50% flowering (Table 6). The crosses which exhibited highest significant negative *sca* effects for earliness are MUT-2-8-3-2 x M-17-R (-1.805) followed by ARG-6-3-1-4 x GKVK-3 (-1.730) and ARG-2-1-2 x GKVK-2 (-1.580). The parents of best specific combinations, MUT-2-8-3-2 x M-17-R (Table 7) were of low x low general combiners indicating the involvement of non-additive gene action and over dominance in the expression of this trait. With respect to days to maturity, 17 out of 50 crosses manifested significant *sca* effects, of which the highest negative *sca* effect was manifested by ARG 3 x GKVK-2 (-2.545), followed by ARG 3 x LTRR-822 (-2.395) and ARG-2-1-2 x RHA 6D-1 (-2.220). Ghaffari et al. (2020) also obtained similar results and concluded that crosses showing negative significant *sca* effects possess dominant or over dominant type of genes with decreasing effect hence may be exploited for earliness in sunflower.

For plant height, best crosses which exhibited high negative *sca* effect were ARG-6-3-1-4 x GKVK-3 (-15.125) followed by ARG-6-3-1-4 x RHA 6D-1 (-12.465) and ARG 3 x GKVK-2 (-10.265). Bhoite et al. (2018) also reported good specific combiners for plant height. Head diameter in case of sunflower is an important yield attributing character since there is a positive correlation of head size with number of seeds per head and in turn with seed yield. The hybrid MUT-2-8-3-2 x GKVK-3 (1.160) topped the list of crosses which showed highest significant positive *sca* effects followed by ARG-6-3-1-4 x GKVK-2 (0.728) and ARG-6-3-1-4 x MR-1 (0.648). Preponderance of non-additive gene action for this trait was also observed by Parameshwarappa et al. (2008) and Machikowa et al. (2011). Ten out of 50 hybrids showed significant *sca* effect for stem diameter, of which five were in positive and five were in negative direction. The hybrid ARG-6-3-1-4 x GKVK-2 (0.246) expressed significant positive *sca* effect followed by MUT-2-8-3-2 x GKVK-3 (0.141) and ARG 3 x RHA 6D-1 (0.138). Contrary to this, cross ARG 3 x GKVK-2 (-0.254) exhibited highest significant negative *sca* effects followed by ARG-6-3-1-4 x RHA-6D-1 (-0.227). However, the magnitude of *sca* effects among the hybrids was very low for this trait. These results are in confirmation with those observed in the studies of Shankar et al. (2007).

Eight cross combinations showed significant positive *sca* effects for 100 seed weight. Of these, ARG-2-1-2 x RHA 6D-1 (0.535), ARG-6-3-1-4 x GKVK-3 (0.525) and MUT-2-8-3-2 x X-15-NB-10 (0.456) were the best specific combiners. Of the top three ranked hybrid for the trait two crosses involved at least one parent with low *gca* effect i.e., these crosses were of high x low or low x high type of specific combinations suggesting the involvement of non-additive gene action in the inheritance of this trait. Patil et al. (2017) reported good specific combiners for 100 seed weight and also reported existence of non additive gene action in the inheritance of this trait. The cross combination E002 x X-15-NB-10 (2.816) was the best specific combiner for volume weight followed by MUT-2-8-3-2 x MR-1 (2.157) and MUT-2-8-3-2 x LTRR-822 (2.049). All the three best crosses involved at least one parent with low *gca* effects, clearly suggesting the involvement of non-additive gene action in the inheritance of the trait. Similar results were obtained by Chandra et al. (2011) and Lakshman et al. (2019).

With respect to seed yield, *sca* ranged from - 258.81 to 404.04 with the best specific combiner being MUT-2-8-3-2 x GKVK-3 (404.036), followed by ARG-2-1-2 x LTRR-822 (295.926) and E002 x M-17-R (254.425). A large reservoir of variability was evident as could be inferred from the range as well as magnitude and direction of *sca* effects for this character. In the first two top crosses viz., MUT-2-8-3-2 x GKVK-3 and ARG-2-1-2 x LTRR-822, at least one parent with high and other parent with low *gca* effects were present. This could be attributed to the involvement of non-additive gene action. However, it was interesting to note that in the third cross viz., E002 x M-17-R both the parents with low *gca* effects were involved suggesting preponderance of over dominance and epistasis. Dhillon and Tyagi (2016) also reported good specific combiners for seed yield in sunflower.

Thirty five out of 50 crosses showed significant *sca* effects for hull content, of which ARG-2-1-2 x RHA-93 (-4.646) topped the list of hybrids expressing significant negative *sca* effect followed by ARG-6-3-1-4 x M-17-R (-3.588) and ARG-2-1-2 x X-15-NB-10 (-3.501). In contrary, cross MUT-2-8-3-2 x X-15-NB-10 (3.731) and ARG-6-3-1-4 x GKVK 3 (3.648) exhibited highest significant negative *sca* effects. Bhoite et al. (2018) reported desired negative specific combiners

for this trait. With respect to seed filling percentage, fourteen and thirteen crosses exhibited significant positive and negative *sca* effects, respectively. The cross, MUT-2-8-3-2 x RHA 272-II (5.329), ARG-2-1-2 x LTRR-822 (3.556) and ARG-2-1-2 x X-15-NB-10 (2.718) were the best specific combiners for seed filling percentage. Meena et al. (2013) and Sharma and Shadakshari (2021) also reported good specific combiners for seed filling percentage.

Highly significant *sca* effects for oil content were observed in thirty nine crosses, of which nineteen and twenty crosses expressed positive and negative significant *sca* effects, respectively. The hybrids E002 x X-15-NB-10 (2.520), MUT-2-8-3-2 x GKVK-3 (2.070) and ARG-2-1-2 x RHA-93 (1.961) topped the list of crosses expressing significant positive *sca* effects. The best specific combination E002 x X-15-NB-10 was having parents with low combining ability which indicated the involvement of non-additive gene action and also existence of over dominance and epistasis in the inheritance of this trait. With reference to oil yield, hybrids viz., MUT-2-8-3-2 x GKVK-3 (171.895) followed by ARG-2-1-2 x LTRR-822 (98.581) and MUT-2-8-3-2 x RHA-93 (72.726) were the best specific combiners among 50 hybrids. Top ranking hybrids had atleast one parent with low combining ability type of parental combinations suggesting the action of non additive gene in the inheritance of this trait. Non additive gene action for oil content and oil yield was also reported by Azad et al. (2016) and Hilli et al. (2020). None of the hybrids were good specific combiners for all the characters studied. However, the cross combination MUT-2-8-3-2 x GKVK 3 was found to be good specific combiner for stem diameter, 100 seed weight, seed yield, seed filling percentage, oil content and oil yield hence it can be tested in large scale yield trials over locations and seasons to confirm its potentiality for commercial cultivation. As these hybrids are based on diverse cytotsterile sources, even their on par performance with PET 1 cytoplasm based hybrids will be sufficient enough so that the cytoplasmic base of sunflower hybrids can be expanded.

Variance due to general and specific combining ability effects

The ratio of *GCA* to *SCA* is used to indicate the predominance of non-additive gene action in the inheritance of the traits. The results revealed that, among the twelve characters studied, characters viz., days to 50% flowering, plant height, days to maturity and volume weight there was preponderance of additive gene action as indicated by greater than unity *GCA* to *SCA* ratio (Table 8), while remaining characters viz., head diameter, stem diameter, 100 seed weight, seed yield, hull content, seed filling percent, oil content and oil yield manifested a higher magnitude of *SCA* variance as compared to *GCA* variance. Similar to the present findings, non-additive gene actions were documented for head diameter (cm), stem diameter (cm), 100 seed weight (g), seed yield (kg/ha), hull content (%), seed filling percent, oil content (%), and oil yield (kg/ha) by Bhoite et al. (2018) and Hilli et al. (2020).

Proportional contribution of lines, testers and line x tester interaction for the performance of hybrids

The data on the proportional contribution of lines, testers and line x tester interaction for twelve quantative traits revealed that the line x tester interaction contributed more for the performance of hybrids for most of the characters such head diameter, stem diameter, 100 seed weight, seed yield, hull content, seed filling percent, oil content and oil yield (Table 9). However, for days to 50% flowering, days to maturity and volume weight contribution of the testers was more when compared to lines and line x tester interaction. Shankar et al. (2007) observed similar results and emphasized that due care needs to be excised while selecting the inbreds/lines to be used as parents for hybridization and to safely use these sources to broaden the genetic base of CMS source so that this valuable oilseed crop can be safeguarded from any eventuality of biotic and abiotic threats in future.

Table 6: Estimates of specific combing ability effects of crosses for seed yield and its attributing traits sunflower.

Hybrids	Days to 50% flowering	Plant height (cm)	Head diameter (cm)	Stem diameter (cm)	Days to maturity	100 seed weight (g)	Volume weight (g/100ml)	Seed yield (Kg/ha)	Hull content (%)	Seed filling percent	Oil content (%)	Oil yield (Kg/ha)
ARG-2-1-2 x GKVK-3	-0.330	0.048	-0.335	-0.019	-0.570	-0.119	-0.020	-244.963 *	0.491	-2.268 **	-1.104 **	-104.931 **
ARG-2-1-2 x RHA 6D-1	-0.230	-0.793	0.530 *	0.109 *	-2.220 **	0.535 **	0.589	6.281	0.928	-0.087	0.681 **	11.969
ARG-2-1-2 x 95-C-1	-0.330	-0.002	-0.030	-0.040	-1.970 **	0.413 **	-0.377	62.870	-0.784	1.233 *	-1.073 **	6.120
ARG-2-1-2 x LTRR-822	-0.080	-3.123	0.060	0.011	0.980	0.217	1.416	295.926 **	-2.097 **	3.556 **	-0.457 *	98.581 **
ARG-2-1-2 x M-17-R	1.770 **	-10.118 **	-0.475 *	0.010	0.930	-0.220	-0.305	-180.030	1.424 **	1.058	0.771 **	-57.825
ARG-2-1-2 x MR-1	0.420	3.178	-0.060	0.051	0.230	-0.350 *	0.741	-145.797	0.924	-2.747 **	1.047 **	-30.002
ARG-2-1-2 x RHA 272-II	0.620	-0.283	0.080	-0.015	2.580 **	0.074	-0.504	136.325	1.335 **	0.863	-1.429 **	16.296
ARG-2-1-2 x X-15-NB-10	0.470	7.347 *	-0.165	-0.012	1.480 *	-0.633 **	-1.746	-98.575	1.393 *	-2.081 **	0.155	-34.101
ARG-2-1-2 x GKVK-2	-1.580 **	5.183	0.220	-0.073	-0.670	-0.038	0.771	99.481	1.030 *	-1.739 **	-0.550 **	23.351
ARG-2-1-2 x RHA-93	-0.730	-1.438	0.175	-0.018	-0.770	0.122	-0.563	68.481	-4.646 **	2.213 **	1.961 **	70.540
MUT-2-8-3-2 x GKVK-3	-0.405	1.830	1.160**	0.141 **	-0.820	0.395 **	0.626	404.036 **	-2.191 **	1.932 **	2.070 **	171.895 **
MUT-2-8-3-2 x RHA 6D-1	0.945	3.665	-0.025	-0.056	0.530	-0.453 **	0.427	-205.830	1.754 **	-1.804 **	-1.771 **	-94.955 **
MUT-2-8-3-2 x 95-C-1	-0.905	-1.970	-0.585 *	0.015	-1.220	0.268	-0.376	-0.352	0.0001	-2.994 **	0.285	-0.152
MUT-2-8-3-2 x LTRR-822	-0.905	-0.765	-0.045	-0.031	-2.020 **	-0.041	2.049 *	-130.075	-1.973 **	0.704	-1.271 **	-67.103
MUT-2-8-3-2 x M-17-R	-1.805 **	-7.210 *	-0.405	-0.070	-0.570	-0.565 **	-1.094	-258.808 *	-2.120 **	-4.747 **	-0.128	-77.874 *
MUT-2-8-3-2 x MR-1	-0.155	-8.965 **	-0.390	-0.032	0.230	-0.076	2.157 *	65.703	-0.023	0.746	-0.562 **	3.896
MUT-2-8-3-2 x RHA 272-II	0.545	5.175	-0.200	0.017	0.580	0.241	0.637	65.881	3.398 **	5.329 **	0.312	34.445
MUT-2-8-3-2 x X-15-NB-10	-0.355	-4.945	0.380	-0.082	-0.520	0.456 **	-1.847 *	99.037	3.731 **	-1.058	-0.732 **	20.172
MUT-2-8-3-2 x GKVK-2	3.095 **	7.265 *	-0.135	0.027	2.830 **	-0.463 **	-1.723	-225.130 *	-3.062 **	0.714	0.579 **	-63.050

Hybrids	Days to 50% flowering	Plant height (cm)	Head diameter (cm)	Stem diameter (cm)	Days to maturity	100 seed weight (g)	Volume weight (g/100ml)	Seed yield (Kg/ha)	Hull content (%)	Seed filling percent	Oil content (%)	Oil yield (Kg/ha)
		5.920	0.245	0.072			-0.857	185.537	0.485		1.217 **	72.726 *
MUT-2-8-3-2 x RHA-93	-0.055				0.980	0.236				1.176 *		
E002 x GKVK-3	0.745	10.748 **	0.070	0.031	0.230	-0.212	-0.485	-135.508	-1.006 *	-1.744 **	0.631 **	-28.960
E002 x RHA 6D-1	-0.905	5.708	-0.240	0.037	-1.670 *	-0.065	-1.437	3.403	-0.401	1.428 *	0.326	4.908
E002 x 95-C-1	-0.255	1.447	0.200	0.048	-0.170	-0.020	0.328	14.270	1.410 **	0.575	-2.151 **	-37.474
E002 x LTRR-822	0.495	-0.372	0.065	0.019	2.280 **	-0.089	-2.098 *	-72.397	0.062	-2.250 **	1.218 **	-4.715
E002 x M-17-R	-0.405	1.658	0.305	-0.125 **	-1.520 *	0.300 *	1.825 *	254.425 *	1.818 **	1.370 *	-1.579 **	57.106
E002 x MR-1	0.495	-4.298	-0.030	-0.039	0.530	0.312 *	-1.912 *	-9.952	0.327	-0.035	-0.465 *	-11.184
E002 x RHA 272-II	-1.055	-5.383	-0.190	-0.135 **	-0.870	-0.019	0.278	40.225	-1.262 **	-4.392 **	1.276 **	38.730
E002 x X-15-NB-10	-0.205	-1.753	0.015	0.076	-0.220	-0.101	2.816 **	-26.619	-2.401 **	2.718 **	2.520 **	38.415
E002 x GKVK-2	0.745	-5.293	-0.075	0.055	1.130	0.264	-0.072	76.992	0.173	2.438 **	-0.072	25.695
E002 x RHA-93	0.345	-2.463	-0.120	0.035	0.280	-0.371 *	0.759	-144.841	1.280 **	-0.110	-1.704 **	-82.519 *
ARG 3 x GKVK-3	1.720 **	2.500	0.358	0.035	2.555 **	-0.589 **	-1.159	104.920	-0.943 *	1.901 **	0.080	36.993
ARG 3 x RHA 6D-1	0.320	3.885	0.348	0.138 **	4.405 ***	0.098	-0.583	126.998	1.142 *	1.403 *	-0.433 *	32.683
ARG 3 x 95-C-1	0.470	-6.375 *	0.262	-0.021	1.155	-0.231	0.289	-74.469	1.998 **	1.120	1.176 **	-5.127
ARG 3 x LTRR-822	0.470	-0.820	-0.147	-0.050	-2.395 **	-0.103	-1.127	-28.635	2.177 **	0.400	-0.600 **	-22.813
ARG 3 x M-17-R	-0.180	4.985	0.442	0.136 *	-0.445	0.228	0.246	104.909	2.466 **	1.710 **	1.052 **	56.169
ARG 3 x MR-1	-1.280 *	-0.420	-0.167	-0.038	-1.895 **	-0.095	-0.604	-9.802	-1.647 **	-0.480	-0.056	-6.531
ARG 3 x RHA 272-II	-0.830	3.345	-0.027	0.061	-1.545 *	-0.095	0.041	-87.402	-2.341 **	-2.137 **	1.047 **	-4.180
ARG 3 x X-15-NB-10	0.020	1.300	-0.223	0.002	0.355	0.220	1.932 *	-13.969	-3.501 **	-0.019	-0.361	-7.055
ARG 3 x GKVK-2	-1.530 **	-10.265 **	-0.738 **	-0.254 **	-2.545 **	0.210	0.391	-4.802	0.394	-1.052	0.622 **	8.440
ARG 3 x RHA-93	0.820	1.865	-0.107	-0.009	0.355	0.355 *	0.572	-117.747	0.256	-2.848 **	-2.528 **	-88.579 *
ARG-6-3-1-4 x GKVK-3	-1.730**	-15.125 **	-1.253 **	-0.187 *	-1.395	0.525 **	1.038	-128.486	3.648 **	0.178	-1.678 **	-74.997 *

Hybrids	Days to 50% flowering	Plant height (cm)	Head diameter (cm)	Stem diameter (cm)	Days to maturity	100 seed weight (g)	Volume weight (g/100ml)	Seed yield (Kg/ha)	Hull content (%)	Seed filling percent	Oil content (%)	Oil yield (Kg/ha)
ARG-6-3-1-4 x RHA 6D-1	-0.130	-12.465 **	-0.613 **	-0.227 **	-1.045	-0.116	1.004	69.148	-3.424 **	-0.941	1.197 **	45.395
ARG-6-3-1-4 x 95-C-1	1.020	6.900 *	0.153	0.001	2.205 **	-0.430**	0.136	-2.319	-2.624 **	0.064	1.763 **	36.633
ARG-6-3-1-4 x LTRR-822	0.020	5.080	0.068	0.051	1.155	0.016	-0.240	-64.819	1.831 **	-2.411 **	1.109 **	-3.950
ARG-6-3-1-4 x M-17-R	0.620	10.685 **	0.132	0.049	1.605 *	0.257	-0.672	79.504	-3.588 **	0.609	-0.116	22.424
ARG-6-3-1-4 x MR-1	0.520	10.505 **	0.648 **	0.058	0.905	0.209	-0.382	99.847	0.419	2.514 **	0.036	43.821
ARG-6-3-1-4 x RHA 272-II	0.720	-2.855	0.338	0.072	-0.745	-0.202	-0.452	-155.030	-1.130 *	0.337	-1.206 **	-85.290 *
ARG-6-3-1-4 x X-15-NB-10	0.070	-1.950	-0.008	0.017	-1.095	0.058	-1.156	40.126	0.778	0.440	-1.582 **	-17.430
ARG-6-3-1-4 x GKVK-2	-0.730	3.110	0.728 **	0.246 **	-0.745	0.026	0.633	53.459	1.465 **	-0.361	-0.579 **	5.565
ARG-6-3-1-4 x RHA-93	-0.380	-3.885	-0.193	-0.079	-0.845	-0.342 *	0.089	8.570	2.624 **	-0.431	1.054 **	27.831
SE±	0.536	3.210	0.226	0.042	0.714	0.144	0.896	104.899	0.470	0.575	0.205	35.633

** significant at $P \leq 0.01$ * significant at $P \leq 0.05$

Table 7: Top ranking hybrids with high *sca* effects in desirable direction for seed yield and its component traits in sunflower.

Rank	Days to 50% flowering	Rank	Plant height (cm)
1	MUT-2-8-3-2 x M-17-R	1	ARG-6-3-1-4 x GKVK-3
2	ARG-6-3-1-4 x GKVK-3	2	ARG-6-3-1-4 x RHA 6D-1
3	ARG-2-1-2 x GKVK-2	3	ARG 3 x GKVK-2
4	ARG 3 x GKVK-2	4	ARG-2-1-2 x M-17-R
5	ARG 3 x MR-1	5	MUT-2-8-3-2 x MR-1
Rank	Head diameter (cm)	Rank	Stem diameter (cm)
1	MUT-2-8-3-2 x GKVK-3	1	ARG-6-3-1-4 x GKVK-2
2	ARG-6-3-1-4 x GKVK-2	2	MUT-2-8-3-2 x GKVK-3
3	ARG-6-3-1-4 x MR-1	3	ARG 3 x RHA 6D-1
4	ARG-2-1-2 x RHA 6D-1	4	ARG 3 x M-17-R
5	ARG 3 x M-17-R	5	ARG-2-1-2 x RHA 6D-1
Rank	Days to maturity	Rank	100 seed weight (g)
1	ARG 3 x GKVK-2	1	ARG-2-1-2 x RHA 6D-1
2	ARG 3 x LTRR-822	2	ARG-6-3-1-4 x GKVK-3
3	ARG-2-1-2 x RHA 6D-1	3	MUT-2-8-3-2 x X-15-NB-10
4	MUT-2-8-3-2 x LTRR-822	4	ARG-2-1-2 x 95-C-1
5	ARG-2-1-2 x 95-C-1	5	MUT-2-8-3-2 x GKVK-3
Rank	Volume weight (g/100ml)	Rank	Seed yield(kg/ha)
1	E002 x X-15-NB-10	1	MUT-2-8-3-2 x GKVK-3
2	MUT-2-8-3-2 x MR-1	2	ARG-2-1-2 x LTRR-822
3	MUT-2-8-3-2 x LTRR-822	3	E002 x M-17-R
4	ARG 3 x X-15-NB-10	4	MUT-2-8-3-2 x RHA-93
5	E002 x M-17-R	5	ARG-2-1-2 x RHA 272-II
Rank	Hull content (%)	Rank	Seed filling per-cent
1	ARG-2-1-2 x RHA-93	1	MUT-2-8-3-2 x RHA 272-II
2	ARG-6-3-1-4 x M-17-R	2	ARG-2-1-2 x LTRR-822
3	ARG-2-1-2 x X-15-NB-10	3	ARG-2-1-2 x X-15-NB-10
4	ARG-6-3-1-4 x RHA 6D-1	4	ARG-6-3-1-4 x MR-1
5	MUT-2-8-3-2 x GKVK-2	5	E002 x GKVK-2
Rank	Oil content (%)	Rank	Oil yield (kg/ha)
1	E002 x X-15-NB-10	1	MUT-2-8-3-2 x GKVK-3
2	MUT-2-8-3-2 x GKVK-3	2	ARG-2-1-2 x LTRR-822
3	ARG-2-1-2 x RHA-93	3	MUT-2-8-3-2 x RHA-93
4	ARG-6-3-1-4 x 95-C-1	4	ARG-2-1-2 x RHA-93
5	E002 x RHA 272-II	5	E002 x M-17-R

Table 8: Variance due to general and specific combining ability effects for seed yield and its attributing traits in sunflower.

Characters	Variance due to GCA	Variance due to SCA	GCA/ SCA
Days to 50% flowering	2.456	0.877	2.800
Plant height (cm)	62.160	35.930	1.730
Head diameter (cm)	0.048	0.158	0.304
Stem diameter (cm)	0.002	0.009	0.222
Days to maturity	3.285	2.594	1.266
100 seed weight (g)	0.049	0.100	0.490
volume weight (g/100ml)	3.057	0.875	3.494
Seed yield (kg/ha)	8422.689	13879.046	0.607
Hull content (%)	2.241	5.314	0.422
Seed filling (%)	3.177	5.083	0.625
Oil content (%)	1.850	7.344	0.252
Oil yield (kg/ha)	2681.516	6346.924	0.422

Table 9: Proportional contribution of lines, testers and L x T interaction to the total variance among the hybrids.

Sl. No.	Characters	Lines (L)	Testers (T)	L x T interaction
1	Days to 50% flowering	28.730	56.228	15.042
2	Plant height (cm)	39.842	35.814	24.344
3	Head diameter (cm)	13.012	28.252	58.736
4	Stem diameter (cm)	3.950	35.319	60.732
5	Days to maturity	26.322	47.364	26.314
6	100 seed weight (g)	27.379	21.159	51.462
7	volume weight (g/100ml)	28.199	55.045	16.756
8	Seed yield (kg/ha)	18.907	31.451	49.643
9	Hull content (%)	27.589	19.434	52.977
10	Seed filling (%)	28.229	29.903	41.868
11	Oil content (%)	4.622	13.035	82.344
12	Oil yield (kg/ha)	12.477	24.827	62.696

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Figures

Figure 1

Diversified CMS line E002

Figure 2

Diversified CMS line ARG-3

Figure 3

Diversified CMS line ARG 2-1-2

Figure 4

Diversified CMS line ARG 6-3-1-4

Figure 5

Diversified CMS line MUT2 8-3-2

Figure 6

General View of experimental plot.

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